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AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1.   (currently amended) A computerized method for determining whether a biological sequence has certain ~~characteristic~~ orientation comprising:

obtaining a plurality of evidence about the ~~characteristic~~ orientation, wherein at least one evidence is sequence annotation; and

determining the ~~characteristic~~ orientation using a Bayesian analysis of the evidence.

2.   (currently amended) The method of Claim 1 wherein the step of determining the orientation comprises:

defining ~~the~~ a prior probability of an hypothesis that the biological sequence having the ~~characteristic~~ said orientation;

estimating ~~the~~ a probability of the evidence assuming the hypothesis is true; and

calculating ~~the~~ a probability that the hypothesis is true.

3.   (original) The method of Claim 2 wherein the step of calculating is performed according the Bayes' rule.

4.   (currently amended) The method of Claim 3 wherein the biological sequence is a nucleic acid sequence ~~and the characteristic is the orientation of the biological sequence~~.

5.   (original) The method of Claim 4 wherein the nucleic acid sequence represents a cluster of nucleic acid sequences including at least one EST sequence.

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6.   (original) The method of Claim 5 wherein the plurality of evidence comprises evidence form poly-A/T tail analysis, inferred splice sites and external sequence annotation.

7.   (original) The method of Claim 6 wherein the external sequence annotation comprises RNA label and EST label.

8.   (original) The method of Claim 7 further comprising testing a null hypothesis that the orientation determination is correct and conflicting evidence observed is due to random error.

9.   (withdrawn) A computerized method for designing nucleic acid probe arrays comprising:

    obtaining a plurality of evidence about at least one characteristic of a target nucleic acid sequence, wherein at least one evidence is sequence annotation;

    determining the characteristic using a Bayesian analysis of the evidence; and

    defining a target region based upon the characteristic; and

    selecting probes against the target region.

10.   (withdrawn) The method of Claim 9 wherein the steps of determining comprises defining the prior probability that a hypothesis that the target nucleic acid sequence has the characteristic; estimating the probability of the evidence assuming the hypothesis is true; and

calculating the probability that the hypothesis is true.

11.   (withdrawn) The method of Claim 10 wherein the step of calculating is performed according the Bayes' rule.

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12.   (withdrawn) The method of Claim 11 wherein the characteristic is the orientation of the biological sequence.

13.   (withdrawn) The method of Claim 12 wherein the nucleic acid sequence represents a cluster of nucleic acid sequences including at least one EST sequence.

14.   (withdrawn) The method of Claim 13 wherein the plurality of evidence comprises evidence form poly-A/T tail analysis, inferred splice sites and external sequence annotation.

15.   (withdrawn) The method of Claim 14 wherein the external sequence annotation comprises RNA label and EST label.

16.   (withdrawn) The method of Claim 15 further comprising testing a null hypothesis that the orientation determination is correct and conflicting evidence observed is due to random error.

17.   (currently amended) A system for ~~characterizing~~ determining a biological sequence's orientation comprising a processor; and a memory coupled with the processor, the memory storing a plurality of machine instructions that cause the processor to perform logical steps of:

obtaining a plurality of evidence about the ~~characteristic~~ orientation, wherein at least one evidence is sequence annotation; and

determining the ~~characteristic~~ orientation using a Bayesian analysis of the evidence.

18.   (currently amended) The system of Claim17 wherein the step of determining the orientation comprises:

defining ~~the~~ a prior probability of an hypothesis that the biological sequence having ~~the~~ ~~characteristic~~ said orientation;

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estimating ~~the~~ a probability of the evidence assuming the hypothesis is true; and

calculating ~~the~~ a probability that the hypothesis is true.

19.   (original) The system of Claim 18 wherein the step of calculating is performed

according the Bayes' rule.

20.   (currently amended) The system of Claim 19 wherein the biological sequence is

a nucleic acid sequence ~~and the characteristic is the orientation of the biological~~

~~sequence~~.

21.   (original) The system of Claim 20 wherein the nucleic acid sequence represents a

cluster of nucleic acid sequences including at least one EST sequence.

22.   (currently amended) The system of Claim ~~22~~ 21 wherein the plurality of evidence

comprises evidence form poly-A/T tail analysis, inferred splice sites and external

sequence annotation.

23.   (original) The system of Claim 22 wherein the external sequence annotation

comprises RNA label and EST label.

24.   (original) The system of Claim 23 further comprising testing a null hypothesis

that the orientation determination is correct and conflicting evidence observed is due to

random error.

25.   (withdrawn) A system for characterizing a biological sequence comprising a

processor; and a memory coupled with the processor, the memory storing a plurality of

machine instructions that cause the processor to perform logical steps of:

obtaining a plurality of evidence about at least one characteristic of a target nucleic acid

sequence, wherein at least one evidence is sequence annotation;

determining the characteristic using a Bayesian analysis of the evidence;

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defining a target region based upon the characteristic; and

selecting probes against the target region.

26. (withdrawn) The system of Claim 25 wherein the steps of determining comprises

defining the prior probability that a hypothesis that the target nucleic acid sequence has

the characteristic; estimating the probability of the evidence assuming the hypothesis is

true; and

calculating the probability that the hypothesis is true.

27. (withdrawn) The system of Claim 26 wherein the step of calculating is performed

according the Bayes' rule.

28. (withdrawn) The system of Claim 27 wherein the characteristic is the orientation

of the biological sequence.

29. (withdrawn) The method of Claim 28 wherein the nucleic acid sequence

represents a cluster of nucleic acid sequences including at least one EST sequence.

30. (withdrawn) The system of Claim 29 wherein the plurality of evidence comprises

evidence form poly-A/T tail analysis, inferred splice sites and external sequence

annotation.

31. (withdrawn) The system of Claim 30 wherein the external sequence annotation

comprises RNA label and EST label.

32. (withdrawn) The system of Claim 31 further comprising testing a null hypothesis

that the orientation determination is correct and conflicting evidence observed is due to

random error.

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